| Changed a file from non-ASCII to ASCII ENTERED Changed the margins in cases where the sequence text was "wrapped" down to the next lin. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: | - | CRF Enter Corrected by the STIC System Paranch CRF Processing Dat: 4/16/2002 |
|--|---|---|
| Changed the margins in cases where the sequence text was "wrapped" down to the next lin Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: 2207 guitable; Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other: | N | umb r: 07/00 f, 2/0/1 Fdited by: \(\Lambda\) |
| Changed the margins in cases where the sequence text was "wrapped" down to the next lin Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: 2207 guitable; Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other: | | Changed a file from non-ASCII to ASCII ENTERED (STIC sta |
| Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: \(\alpha \) 22.07 garbage Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: | | |
| applicant was | | Edited a format error in the Current Application Data section, specifically: |
| Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII garbage* at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: Other: | | |
| Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: 2207 | | Added the mandatory heading and subheadings for "Current Application Data". |
| Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: 2207 gallally. Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: | | Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. |
| Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error true to a Patentin bug). Sequences corrected: | , | Changed the spelling of a mandatory field (the headings or subheadings), specifically: |
| Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: 20 gladely. Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: | | Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: |
| applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other: | | Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: |
| Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as | | |
| Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: Z207 | | Inserted colons after headings/subheadings. Headings edited included: |
| Inserted mandatory headings, specifically: | | Deleted extra, invalid, headings used by an applicant, specifically: |
| Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: Other: | | Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as |
| Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: Other: | | Inserted mandatory headings, specifically: <u>C2207 globally</u> |
| Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted <i>ending</i> stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: Other: | | |
| A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted <i>ending</i> stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: | | Edited identifiers where upper case is used but lower case is required, or vice versa. |
| Deleted <i>ending</i> stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a Patentin bug). Sequences corrected: Other: | | Corrected an error in the Number of Sequences field, specifically: |
| due to a Patentin bug). Sequences corrected: | | A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. |
| Other: | | Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: |
| | | Other: |
| | | · |
| | | |

*Examiner: The above corrections must be communicated to the applicant in the first Offic Action. DO NOT send a copy of this form.

Input Set : A:\-80-1.app

```
75
252 65
                         70
                                                                       288
254 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg
255 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
                     85
                                         90
                                                                       336
258 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg
259 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
                100
                                    105
262 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag
                                                                       384
263 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
264
            115
                                120
                                                                       396
266 gga ccc ccg gcc
267 Gly Pro Pro Ala
        130
271 <210> SEQ ID NO: 4
272 <211> LENGTH: 132
273 <212> TYPE: PRT
274 <213> ORGANISM: Mycobacterium tuberculosis
275 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
277 <400> SEQUENCE: 4
278 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe
                                         10
280 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
                                     2.5
282 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
            35
284 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
                             55
286 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
                        70
288 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
290 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
                                    105
292 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
293
                                120
           115
294 Gly Pro Pro Ala
       130
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 702
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <221> NAME/KEY: CDS
305 <222> LOCATION: (4)..(696)
306 <223> OTHER INFORMATION: Ral2-DPPD fusion polypeptide
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence: Ra12-DPPD fusion
        polypeptide
312 <400> SEQUENCE: 5
```



1600

RAW SEQUENCE LISTING DATE: 04/16/2002 PATENT APPLICATION: US/09/684,215A TIME: 11:24:16

Input Set : A:\PTO.AMC.txt

```
3 <110> APPLICANT: Skeiky, Yasir
        Guderian, Jeffrey
        Corixa Corporation
 7 <120> TITLE OF INVENTION: Methods of Using a Mycobacterium tuberculosis Coding
        Sequence to Facilitate Stable and High Yield Expression
8
        of Heterologous Proteins
11 <130> FILE REFERENCE: 014058-008010US
13 <140> CURRENT APPLICATION NUMBER: US 09/684,215A
14 <141> CURRENT FILING DATE: 2000-10-06
16 <150> PRIOR APPLICATION NUMBER: US 60/158,585
17 <151> PRIOR FILING DATE: 1999-10-07
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1872
25 <212> TYPE: DNA
26 <213> ORGANISM: Mycobacterium tuberculosis
28 <220> FEATURE:
29 <223> OTHER INFORMATION: 32 KD serine protease MTB32A
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (89)..(1156)
34 <223> OTHER INFORMATION: MTB32A
36 <220> FEATURE:
37 <221> NAME/KEY: sig_peptide
38 <222> LOCATION: (89)..(184)
39 <223> OTHER INFORMATION: N-terminal hydrophobic secretory signal sequence
41 <220> FEATURE:
42 <221> NAME/KEY: mat_peptide
43 <222> LOCATION: (185)..(1153)
45 <400> SEQUENCE: 1
46 gactacgttg gtgtagaaaa atcctgccgc ccggaccctt aaggctggga caatttctga 60
48 tagctacccc gacacaggag gttacggg atg agc aat tcg cgc cgc cgc tca
                                                                    112
                                 Met Ser Asn Ser Arg Arg Arg Ser
49
                                         -30
50
52 ctc agg tgg tca tgg ttg ctg agc gtg ctg gcc gtc ggg ctg ggc
                                                                    160
53 Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
                   -20
                                      -15
208
57 Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
               - 5
                               -1
60 cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc
                                                                    256
61 Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val
```

Input Set : A:\PTO.AMC.txt

| 62 | 10 | | | | | 15 | | | | | 20 | | | | | |
|-------|----------|-------|-------|-------|-------|---------|-------|-------|-----|----------------|------|--------|-------|-------|------------|------|
| | c caa | | | | | | | | | | | | | | | 304 |
| 65 Al | a Gln | Val | Gly | Pro | Gln | Val | Val | Asn | Ile | Asn | Thr | Lys | Leu | Gly | ${	t Tyr}$ | |
| 66 2 | 5 | | | • | 30 | | | | | 35 | | | | | 40 | |
| 68 aa | c aac | gcc | gtg | ggc | gcc | ggg | acc | ggc | atc | gtc | atc | gat | ccc | aac | ggt | 352 |
| 69 As | n Asn | Ala | Val | Gly | Ala | Gly | Thr | Gly | Ile | Val | Ile | Asp | Pro | Asn | Gly | |
| 70 | | | | 45 | | _ | | _ | 50 | | | _ | | 55 | _ | |
| 72 qt | c gtg | ctq | acc | aac | aac | cac | gtg | atc | qcq | qqc | qcc | acc | qac | atc | aat | 400 |
| | l Val | | | | | | | | | | | | | | | |
| 74 | | | 60 | | | | | 65 | | 1 | | | 70 | | | |
| | g ttc | age | | aac | tcc | aac | caa | | tac | aac | atc | gat | | atc | aaa | 448 |
| | a Phe | | | | | | | | | | | | | | | |
| 78 | .u : 110 | 75 | Vul | OLY | UCI | 013 | 80 | T 111 | -1- | O ₁ | vui | 85 | VUI | Vul | 017 | |
| | t gac | | 200 | 020 | ant. | ata | | ata | ata | C2C | ata | | aat | ~~~ | aa+ | 496 |
| | r Asp | | | | | | | | | | | | | | | 430 |
| _ | _ | AIG | 1111 | GIII | ASP | | АІА | val | ьец | GIII | | Arg | GIY | нта | GIA | |
| 82 | 90 | | | | | 95 | | | | | 100 | | | | | |
| | c ctg | | | | | | | | | | | | | | | 544 |
| | y Leu | Pro | ser | Ala | | He | GLY | GTĀ | GLY | | Ala | Val | GTĀ | GLu | | |
| 86 10 | | | | | 110 | | | | | 115 | | | | | 120 | |
| | c gtc | | | | | | | | | | | | | | | 592 |
| 89 Va | l Val | Ala | Met | _ | Asn | Ser | Gly | Gly | | Gly | Gly | Thr | Pro | _ | Ala | |
| 90 | | | | 125 | | | | | 130 | | | | | 135 | | |
| | g cct | | | | | | | | | | | | | | | 640 |
| 93 Va | l Pro | Gly | Arg | Val | Val | Ala | Leu | Gly | Gln | Thr | Val | Gln | Ala | Ser | Asp | |
| 94 | | | 140 | | | | | 145 | | | | | 150 | | | |
| 96 tc | g ctg | acc | ggt | gcc | gaa | gag | aca | ttg | aac | ggg | ttg | atc | cag | ttc | gat | 688 |
| 97 Se | r Leu | Thr | Gly | Āla | Glu | Glu | Thr | Leu | Asn | Gly | Leu | Ile | Gln | Phe | Asp | |
| 98 | | 155 | _ | • | | | 160 | | | - | | 165 | | | - | |
| 100 q | cc gc | g ato | c caq | ccc | gat | gat | tco | qqq | qqq | ccc | gto | gto | aac | qqq | cta | 736 |
| | la Ål | | | | | | | | | | | | | | | |
| 102 | 17 | | | | - | 175 | | - | • | | 180 | | | - | | |
| | ga ca | a ata | a atc | aat | ato | r aac | aco | a acc | acc | tco | gat | aac | : ttc | cac | cta | 784 |
| | ly Gl | | | | | | | | | | | | | | | |
| 106 1 | - | | | | 190 | | | | | 195 | - | | | | 200 | |
| | .cc ca | a aa1 | - aaa | r can | | | י מכר | att | | | | r cac | r acc | ato | | 832 |
| | er Gl | | | | | | | | | | | | | | | 002 |
| 110 | CI GI. | n Gr | y Gry | 205 | - | 1110 | . Alu | | 210 | | - 01 | GII | . Alu | 215 | | |
| | + a a a | ~ ~~ | | | | + + 0 0 | + | - ~~ | | | | | + | | | 880 |
| | tc gc | | | | | | | | | | | | | | | 000 |
| | Te AT | a GI | | | : AIG | , ser | СТУ | _ | _ | , ser | PIC |) 1111 | | | s iie | |
| 114 | | | 220 | | | | | 225 | | | | | 230 | | | 000 |
| | gg cc | | | | | | | | | | | | | | | 928 |
| | ly Pr | | | Pne | : ье | і СІУ | | _ | va. | L vai | L AS | | | r GTZ | Asn | |
| 118 | | 235 | | | | | 240 | | | | , | 245 | | | | |
| _ | gc gc | _ | - | | _ | | - | | _ | _ | _ | | _ | _ | | 976 |
| | ly Al | | y Val | . Gln | Arg | | | . Gly | Sei | : Ala | | | ı Ala | Ser | Leu | |
| 122 | 25 | - | | | | 255 | | | | | 260 | | | | | |
| | gc at | | | | | | | | | | | | | | | 1024 |
| | ly Il | e Sei | r Thr | Gly | Asp | Val | . Ile | Thr | Ala | | | Gly | Ala | Pro | | |
| 126 2 | 65 | | | | 270 |) | | | | 275 | 5 | | | | 280 | |

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04162002\1684215A.raw

128 aac tog goo acc gog atg gog gac gog ott aac ggg cat cat coc ggt 1072 129 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly 285 290 132 gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca 1120 133 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr 300 305 136 ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga tttcgtcqcq 1166 137 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala 315 138 140 gataccaccc gccggccggc caattggatt ggcgccagcc gtgattgccg cgtgagcccc 1226 142 cgagttccgt ctcccgtgcg cgtggcatcg tggaagcaat gaacgaggca gaacacagcg 1286 144 tegageacce tecegigeag ggeagteacg tegaaggegg tgtgqtegag cateeggatg 1346 146 ccaaggactt cggcagcgcc gccgccctgc ccgccgatcc gacctggttt aagcacgccg 1406 148 tettetaega ggtgetggte egggegttet tegaegeeag egeggaeggt teeggegate 1466 150 tgcgtggact catcgatcgc ctcgactacc tgcagtggct tggcatcgac tgcatctggt 1526 152 tgccgccgtt ctacgactcg ccgctgcgcg acggcggtta cgacattcgc gacttctaca 1586 154 aggtgetgee egaattegge accgtegaeg atttegtege eetggtegae geegeteaee 1646 156 ggcgaggtat ccgcatcatc accgacctgg tgatgaatca cacctcggag tcgcacccct 1706 158 ggtttcagga gtcccgccgc gacccagacg gaccgtacgg tgactattac gtgtqqaqcq 1766 160 acaccagega gegetacace gaegeeegga teatettegt egacacegaa gagtegaact 1826 162 ggtcattcga tcctgtccgc cgacagttct actggcaccg attctt 165 <210> SEQ ID NO: 2 166 <211> LENGTH: 355 167 <212> TYPE: PRT 168 <213> ORGANISM: Mycobacterium tuberculosis 170 <220> FEATURE: 171 <223> OTHER INFORMATION: 32 KD serine protease MTB32A 173 <400> SEQUENCE: 2 174 Met Ser Asn Ser Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser 10 176 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala 177 20 25 178 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu 40 180 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val 181 50 182 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr 183 65 70 75 184 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val 186 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln 100 105 188 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala 189 115 120 125 190 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly 135 192 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly 150 155 194 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu

Input Set : A:\PTO.AMC.txt

| 195 | | | | | 165 | | | | | | | | | | | | |
|--|--|--|--|---|--|--|--|------------------------------------|---|--|--|--|--|--|--|--|-----------------|
| 100 | | | m1 | | 165 | | _ | _ | _ | 170 | | | | | 175 | | |
| 196 | GIA | GIn | Thr | Val | GIn | Ala | Ser | Asp | | Leu | Thr | Gly | Ala | Glu | Glu | Thr | |
| 197 | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 198 | Leu | Asn | Gly | Leu | Ile | Gln | Phe | Asp | Ala | Ala | Ile | Gln | Pro | Gly | Asp | Ser | |
| 199 | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 200 | Gly | Gly | Pro | Val | Val | Asn | Gly | Leu | Glv | Gln | Val | Val | Glv | Met | Asn | Thr | |
| 201 | | 210 | | | | | 215 | | 4 | | | 220 | 0-1 | | | - · · · · | |
| 202 | Ala | Ala | Ser | Asp | Asn | Phe | Gln | Len | Ser | Gln | Glv | | Gln | C117 | Dho | λla | |
| 203 | 225 | | | | | 230 | | 204 | 001 | 0111 | 235 | GLY | GIII | GIY | FILE | | |
| | Ile | | Tle | Glv | Gln | | Mot | λΙэ | Tla | 717 | | C1 = | T1. | 3 | a | 240 | |
| 205 | | | | 011 | 245 | niu | Mec | AIG | TTE | | GIY | GIII | тте | Arg | | GIA | |
| | | C1** | 802 | Dvo | | 370 7 | 774 - | T1. | a1 | 250 | -1 | | _, | _ | 255 | | |
| 207 | Gly | Gry | ser | 510 | 1111 | val | HIS | тте | | Pro | Inr | Ala | Phe | | Gly | Leu | |
| | | 77- 1 | **- 1 | 260 | _ | _ | | _ | 265 | _ | | | | 270 | | | |
| 208 | Gly | val | val | Asp | Asn | Asn | GTA | Asn | Gly | Ala | Arg | Val | Gln | Arg | Val | Val | |
| 209 | | | 275 | | | | | 280 | | | | | 285 | | | | |
| 210 | Gly | Ser | Ala | Pro | Ala | Ala | Ser | Leu | Gly | Ile | Ser | Thr | Gly | Asp | Val | Ile | |
| 211 | | 290 | | | | | 295 | | | | | 300 | | | | | |
| 212 | Thr | Ala | Val | Asp | Gly | Ala | ${\tt Pro}$ | Ile | Asn | Ser | Ala | Thr | Ala | Met | Ala | Asp | |
| 213 | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 214 | Ala | Leu | Asn | Gly | His | His | Pro | Gly | Asp | Val | Ile | Ser | Val | Thr | Trp | Gln | |
| 215 | | | | _ | 325 | | | • | • | 330 | | | | | 335 | V 2 | |
| 216 | Thr | Lys | Ser | Glv | Glv | Thr | Ara | Thr | Glv | | Val | Thr | T.e.ii | Δla | Glu | Glw | |
| 217 | | • | | 340 | 2 | | 5 | | 345 | | , | **** | ДСи | 350 | Giu | GLY | |
| 218 | Pro | Pro | Ala | | | | | | 015 | | | | | 330 | | | |
| 219 | | | 355 | | | | | | | | | | | | | | |
| | <210 |)> SI | | NO. | ٦. | | | | | | | | | | | | |
| | <211 | | | | | | | | | | | | | | | | |
| | <212 | | | | , 0 | | | | | | | | | | | | |
| ~ ~ ~ | | | | DNA | | | | | | | | | | | | | |
| | | | | | Mirac | haat | ~~4 | + | h | 7 | | | | | | | |
| 225 | <213 | 3> OF | RGANI | SM: | Мусс | bact | eriu | ım tu | bero | ulos | sis | | | | | | |
| 225 227 | <213 <220 | 3> OF 3> FE | RGANI EATUR | SM: RE: | | | | | | | | | | _ | | | |
| 225 227 228 | <213 <220 <223 | 3> OF 3> FE 3> OT | RGANI EATUR CHER | SM: RE: INFO | | | | | | | | agme | ent c | of MI | B32 <i>A</i> | A Ra12 | |
| 225 227 228 230 | <213 <220 <223 <220 | 3> OF 3> FE 3> OT 3> FE | RGANI EATUR PHER EATUR | SM: E: INFO E: | RMAT | | | | | | | agme | ent c | of MI | B32# | A Ra12 | |
| 225 227 228 230 231 | <213 <220 <223 <221 | 3> OF 3> OF 3> OT 3> FE 1> NA | RGANI EATUR CHER EATUR ME/K | SM: E: INFO E: EY: | RMAT | ON: | 14 | | | | | agme | ent c | of MJ | B32# | A Ral2 | |
| 225 227 228 230 231 232 | <213 <220 <223 <220 <221 <222 | 3> OF 3> OF 3> OT 3> FE 1> NA 2> LO | RGANI EATUR PHER EATUR ME/K PCATI | SM: E: INFO E: EY: ON: | CDS | 'ION: | 14 6) | KD C | | | | agme | ent c | of MI | °B32# | A Ral2 | |
| 225 227 228 230 231 232 233 | <213 <220 <223 <221 <222 <223 | 3> OF 3> OF 3> OT 3> FE 1> NA 2> LO 3> OT | RGANI EATUR EATUR ME/K OCATI | SM: E: INFO E: EY: ON: INFO | CDS (1). | 'ION: | 14 6) | KD C | | | | agme | ent c | of MI | B32A | A Ral2 | |
| 225 227 228 230 231 232 233 235 | <213 <220 <223 <221 <222 <223 <400 | 3> OF 3> OF 3> OT 3> FE 1> NA 2> LO 3> OT 3> SE | RGANI EATUR EATUR ME/K OCATI CHER CQUEN | SM: INFO E: EY: ON: INFO | CDS (1). RMAT | 'ION: . (39 'ION: | 14 6) Ra1 | KD C | -ter | rmina | ıl fr | | | | | | |
| 225 227 228 230 231 232 233 235 236 | <213 <220 <223 <220 <221 <222 <223 <400 acg | 3> OF 3> OF 3> OF 3> OF 1> NA 2> LO 3> OF 5> SE gcc | RGANI EATUR EATUR ME/K CATI THER CQUEN GCG | SM: EE: INFO EE: ON: INFO CE: tcc | CDS (1). RMAT 3 gat | ION: .(39 ION: | 14 6) Ral | KD C | :-ter | mina | ıl fr cag | ggt | ggg | caq | qqa | ttc | 48 |
| 225 227 228 230 231 232 233 235 236 | <213 <220 <223 <220 <221 <222 <223 <400 acg | 3> OF 3> OF 3> OF 3> OF 1> NA 2> LO 3> OF 5> SE gcc | RGANI EATUR EATUR ME/K CATI THER CQUEN GCG | SM: EE: INFO EE: ON: INFO CE: tcc | CDS (1). RMAT 3 gat | ION: .(39 ION: | 14 6) Ral | KD C | :-ter | mina | ıl fr cag | ggt | ggg | caq | qqa | ttc | |
| 225 227 228 230 231 232 233 235 236 237 238 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr | 3> OF 3> OF 3> OF 5> FF 1> NA 2> LO 3> OF 5> SE 9CC Ala | RGANI CHER CATUR CATUR CATI CHER CQUEN GCG Ala | SM: E: INFO E: EY: ON: INFO CE: tcc Ser | CDS (1). RMAT 3 gat Asp | .(39 'ION: 'ION: aac Asn | 14 6) Ral ttc Phe | .2 cag Gln | ctg Leu | tcc Ser | cag | ggt Gly | ggg Gly | cag Gln | gga Gly 15 | ttc Phe | |
| 225 227 228 230 231 232 233 235 236 237 238 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr | 3> OF 3> OF 3> OF 5> FF 1> NA 2> LO 3> OF 5> SE 9CC Ala | RGANI CHER CATUR CATUR CATI CHER CQUEN GCG Ala | SM: E: INFO E: EY: ON: INFO CE: tcc Ser | CDS (1). RMAT 3 gat Asp | .(39 'ION: 'ION: aac Asn | 14 6) Ral ttc Phe | .2 cag Gln | ctg Leu | tcc Ser | cag | ggt Gly | ggg Gly | cag Gln | gga Gly 15 | ttc Phe | 48 |
| 225 227 228 230 231 232 233 235 236 237 238 240 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr 1 gcc | 3> OF FE 3> OF FE 3> OF FE 1> NA 2> LO 3> OF 50> SE 9cc Ala att | RGANI EATUR EATUR ME/K ME/K PHER EQUEN GCG Ala | SM: RE: INFO RE: CON: INFO CCE: tcc Ser | CDS (1). PRMAT 3 gat Asp 5 | .(39 ION: aac Asn | 14 6) Ral ttc Phe | KD C | ctg Leu gcg | tcc Ser 10 | cag Gln | ggt Gly | ggg Gly cag | cag Gln atc | gga Gly 15 | ttc Phe tcg | |
| 225 227 228 230 231 232 233 235 236 237 238 240 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr | 3> OF FE 3> OF FE 3> OF FE 1> NA 2> LO 3> OF 50> SE 9cc Ala att | RGANI EATUR EATUR ME/K ME/K PHER EQUEN GCG Ala | SM: RE: INFO RE: ON: INFO CE: tcc ser atc | CDS (1). PRMAT 3 gat Asp 5 | .(39 ION: aac Asn | 14 6) Ral ttc Phe | KD C | ctg Leu gcg Ala | tcc Ser 10 | cag Gln | ggt Gly | ggg Gly cag | cag Gln atc Ile | gga Gly 15 | ttc Phe tcg | 48 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr 1 gcc Ala | 3> OF FE 3> OF FE 3> OF FE 2> LO 3> OF 3> OF 3> OF 3> OF 4 4 4 4 4 4 4 4 4 | RGANI EATUR CHER ME/K CCATI CHER CQUEN GCG Ala CCG Pro | SM: RE: INFO RE: EY: ON: INFO CE: tcc Ser atc Ile 20 | CDS (1). RMAT 3 gat Asp 5 ggg Gly | .(39 'ION: aac Asn cag Gln | 14 6) Ral ttc Phe gcg Ala | Cag Gln atg | ctg Leu gcg Ala 25 | tcc Ser 10 atc | cag Gln gcg Ala | ggt Gly ggc Gly | ggg Gly cag Gln | cag Gln atc Ile 30 | gga Gly 15 cga Arg | ttc Phe tcg Ser | 48 96 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 244 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr 1 gcc Ala | 3> OF FF 3> OF FF 3> OF FF 2> LO 3> OF 3> OF 4> NA 3> OF 4 4 4 4 4 4 4 4 4 | RGANI EATUR EATUR ME/K OCATI CHER GOUEN GCG Ala CCG Pro | SM: EE: INFO EE: EY: ON: INFO CE: tcc Ser atc Ile 20 tca | CDS (1). ORMAT 3 gat Asp 5 ggg Gly ccc | CION: .(39 CION: aac Asn cag Gln acc | 14 6) Ral ttc Phe gcg Ala gtt | Cag Gln atg Met cat | ctg Leu gcg Ala 25 atc | tcc Ser 10 atc Ile | cag Gln gcg Ala | ggt Gly ggc Gly acc | ggg Gly cag Gln | cag Gln atc Ile 30 | gga Gly 15 cga Arg | ttc Phe tcg Ser | 48 96 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 244 245 | <213 <220 <223 <220 <221 <222 <223 <400 acg Thr 1 gcc Ala | 3> OF FF 3> OF FF 3> OF FF 2> LO 3> OF 3> OF 4> NA 3> OF 4 4 4 4 4 4 4 4 4 | RGANI EATUR CHER EATUR ME/K CCATI CHER GQUEN GCG Ala CCG Pro GGG | SM: EE: INFO EE: EY: ON: INFO CE: tcc Ser atc Ile 20 tca | CDS (1). ORMAT 3 gat Asp 5 ggg Gly ccc | CION: .(39 CION: aac Asn cag Gln acc | 14 6) Ral ttc Phe gcg Ala gtt | Cag Gln atg Met Cat | ctg Leu gcg Ala 25 atc | tcc Ser 10 atc Ile | cag Gln gcg Ala | ggt Gly ggc Gly acc | ggg Gly cag Gln gcc Ala | cag Gln atc Ile 30 | gga Gly 15 cga Arg | ttc Phe tcg Ser | 48 96 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 244 245 246 | <213 <220 <223 <221 <222 <223 <400 acg Thr 1 gcc Ala ggt Gly | 3> OF FF SS OF SS | RGANIEATUR CHER CHER CATUR CHER CQUEN GCG Ala CCG Pro GGIY 35 | SM: EE: INFO EE: ON: INFO CE: tcc ser atc Ile 20 tca Ser | CDS (1). ORMAT 3 gat Asp 5 ggg Gly CCC Pro | CION: .(39 CION: aac Asn cag Gln acc Thr | 14 6) Ral ttc Phe gcg Ala gtt Val | Cag Gln atg Met Cat His | ctg Leu gcg Ala 25 atc | tcc Ser 10 atc Ile ggg Gly | cag Gln gcg Ala cct Pro | ggt Gly ggc Gly acc Thr | ggg Gly cag Gln gcc Ala 45 | cag Gln atc Ile 30 ttc Phe | gga Gly 15 cga Arg ctc Leu | ttc Phe tcg Ser ggc Gly | 48 96 144 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 244 245 246 248 | <213 <220 <221 <222 <221 <222 <400 acg Thr 1 gcc Ala ggt Gly | 3> OF 3> OF 3> OF 3> OF 3> OF 3> OF 3> OF 3> OF 4 4 4 5 6 6 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 | RGANIEATURE HER ME/KOCATIE HER GUEN Ala CCG Pro GGly 35 gtt | SM: EE: INFO EE: ON: INFO CE: tcc ser atc Ile 20 tca ser | CDS (1). RMAT 3 gat Asp 5 ggg Gly ccc Pro | CION: .(39 ION: aac Asn cag Gln acc Thr | 14 6) Ral ttc Phe gcg Ala gtt Val | Cag Gln atg Met Cat His 40 ggc | ctg Leu gcg Ala 25 atc Ile | tcc Ser 10 atc Ile ggg Gly | cag Gln gcg Ala cct Pro | ggt Gly ggc Gly acc Thr | ggg Gly cag Gln gcc Ala 45 gtc | cag Gln atc Ile 30 ttc Phe | gga Gly 15 cga Arg ctc Leu | ttc Phe tcg Ser ggc Gly | 48 96 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 244 245 246 248 249 | <213 <220 <223 <221 <222 <223 <400 acg Thr 1 gcc Ala ggt Gly | 3> OF 3> OF 3> OF 3> OF 3> OF 5> OF 5> OF 6> OF 6> OF 6> OF 6> OF 7 8 OF 8 OF 8 OF 8 OF 9 OF 9 OF 9 OF 9 OF 10 OF 11 OF 12 OF 13 OF 14 OF 15 OF 16 OF | RGANIEATURE HER ME/KOCATIE HER GUEN Ala CCG Pro GGly 35 gtt | SM: EE: INFO EE: ON: INFO CE: tcc ser atc Ile 20 tca ser | CDS (1). RMAT 3 gat Asp 5 ggg Gly ccc Pro | CION: .(39 ION: aac Asn cag Gln acc Thr | 14 6) Ral ttc Phe gcg Ala gtt Val aac Asn | Cag Gln atg Met Cat His 40 ggc | ctg Leu gcg Ala 25 atc Ile | tcc Ser 10 atc Ile ggg Gly | cag Gln gcg Ala cct Pro | ggt Gly ggc Gly acc Thr cga Arg | ggg Gly cag Gln gcc Ala 45 gtc | cag Gln atc Ile 30 ttc Phe | gga Gly 15 cga Arg ctc Leu | ttc Phe tcg Ser ggc Gly | 48 96 144 |
| 225 227 228 230 231 232 233 235 236 237 238 240 241 242 244 245 246 248 249 250 | <213 <220 <221 <222 <221 <222 <400 acg Thr 1 gcc Ala ggt Gly | 3> OF 3> OF 3> OF 3> OF 3> OF 5> NA 2> LO 3> OF 3> OF 4 50 QCC Ala att Ile Ggg Gly Ggly 50 | RGANIEATURE THER EATURE AME/KOCATIENER CQUEN Ala CCG Pro Gly 35 gtt Val | SM: EE: INFO EE: EY: ON: INFO CE: tcc ser atc Ile 20 tca Ser yal | CDS (1). RMAT 3 gat Asp 5 ggg Gly ccc Pro gac Asp | CION: .(39 LION: aac Asn cag Gln acc Thr aac | 14 6) Ral ttc Phe gcg Ala gtt Val aac Asn 55 | Cag Gln atg Met cat His 40 ggc Gly | ctg Leu gcg Ala 25 atc Ile aac | tcc Ser 10 atc Ile ggg Gly | cag Gln gcg Ala cct Pro gca Ala | ggt Gly ggc Gly acc Thr cga Arg | ggg Gly cag Gln gcc Ala 45 gtc Val | cag Gln atc Ile 30 ttc Phe caa Gln | gga Gly 15 cga Arg ctc Leu cgc Arg | ttc Phe tcg Ser ggc Gly gtg Val | 48 96 144 |

Input Set : A:\PTO.AMC.txt

```
253 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
254 65
                         70
256 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg
                                                                       288
257 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
                     85
                                         90
260 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg
                                                                       336
261 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
                100
                                    105
264 caa acc aag tog ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag
                                                                       384
265 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
266
            115
                                120
268 gga ccc ccg gcc
                                                                       396
269 Gly Pro Pro Ala
        130
270
273 <210> SEQ ID NO: 4
274 <211> LENGTH: 132
275 <212> TYPE: PRT
276 <213> ORGANISM: Mycobacterium tuberculosis
278 <220> FEATURE:
279 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
281 <400> SEQUENCE: 4
282 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe
284 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
                 20
                                     25
286 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
                                 40
288 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
                             55
290 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
                         70
292 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
293
294 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
               100
                                    105
296 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
           115
                                120
298 Gly Pro Pro Ala
299
      130
302 <210> SEQ ID NO: 5
303 <211> LENGTH: 702
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (4)..(696)
310 <223> OTHER INFORMATION: Ral2-DPPD fusion polypeptide
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Description of Artificial Sequence:Ral2-DPPD fusion
```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/684,215A

DATE: 04/16/2002 TIME: 11:24:17

Input Set : A:\PTO.AMC.txt